

SEQUENCE LISTING

<110> Yamanouchi Pharmaceutical Co., Ltd.

<120> Canine CYP1A2 genetic polymorphism

<130> Y0414PCT-712

<150> JP 2003-152917

<151> 2003-05-29

<150> JP 2003-206581

<151> 2003-08-07

<160> 23

<170> PatentIn version 3.1

<210> 1

<211> 1380

<212> DNA

<213> Canis familiaris

<220>

<223> Inventor: Tenmizu, Daisuke; Fukunaga, Yasuhisa; Noguchi, Kiyoshi

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atgacatata gctgttgtgt gcctaccatg tgtaagccct gggcatacac tggtgcccac 180

ccttgccctag aacatgtgg ggttagggtgg ttactgggcc ttagatata aacagacagt 240

actatgtaat aggggactta gataccatga agcagtcggg gcagccctaa gcccggttt 300

gttttctgtt ttctgcac acggtgattt gcagggcacg gcagccctgc ctctctgaca 360

ggcccccagct gcccttaatg gaggcattca tcctggagat cttctgacac acctcctta 420

tcccccacatccccac aggttaaggcc tgcttcttgc gccttgccac cttttagcc 480

ttcaccatgt ttcttcctcc catcttcata gcccggatc tggctcagac ctccggctct 540

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|---|------|
| catgatcaa ctacccagct ttcaggagaa agtcacactg ctgatcttag ctctcattca    | 660  |
| cctctgtca cattccttgc ctgcaagtac tctcaatcca cccgggctgg cctcgctgta    | 720  |
| cctcccccaggc atgatgcggc caacccaa ttttgcctat gctggacccct ctgcctggaa  | 780  |
| tgcctttaa cctcttctcc caccacactga atcttaccct tgcccaaggta caatcctgac  | 840  |
| acaaacttcc ctttcaactat caggcttct tgactcatcc agctggcaca gtttcaattct  | 900  |
| ctgatgtatt gtaggacttt cagccatttg tccttgatca tgtcctgggc ttttaacaac   | 960  |
| atcaagagac ttagtgaaca tttactctta cccatatgtt ggtctattta ttcccagagt   | 1020 |
| agaaggctcg actcctcagt caggctggga actacccagg gataactccag actgccagg   | 1080 |
| tcttggcttc agaggatggc gaagtgcaca gctggacaca aacaaagggt tagtgaacac   | 1140 |
| ttgctgaagt tgaagaacag aagctgagga agaggaagga tagttcacc cttccgtgc     | 1200 |
| tcctgtatgt ccctcccaact gtaggacata gagactgtgg gggacaaggct attggggtgg | 1260 |
| aagaaggagc aagtagatcc cagagacaca ccccaactgtt cctgccctga gcctgacaga  | 1320 |
| gcctcttcc ctccctcagca caacaaaggaa cacaacctta aagggttctt acatcccaa   | 1380 |

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| <400> 10                      | 18 |
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<213> Artificial Sequence

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<223> Description of Artificial Sequence: an artificially synthesized  
GeneRacer RNA Oligo

<400> 19  
cgacuggagc acgaggacac ugacauggac ugaaggagua gaaa 44

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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: an artificially synthesized  
 GeneRacer 5' primer

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<210> 21  
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<210> 22  
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ag atg gca ttg tcc cag atg gcc aca gag ctt ctc ctg gcc tcc acc 107  
 Met Ala Leu Ser Gln Met Ala Thr Glu Leu Leu Ala Ser Thr  
 1 5 10 15

atc ttc tgc ttg gta ctc tgg gtc aag gcc tgg cag cct cgg ctt 155  
 Ile Phe Cys Leu Val Leu Trp Val Val Lys Ala Trp Gln Pro Arg Leu  
 20 25 30

ccc aaa ggc ctg aag agt cca ccg ggg ccc tgg ggc tgg ccc ctg ctc 203  
 Pro Lys Gly Leu Lys Ser Pro Pro Gly Pro Trp Gly Trp Pro Leu Leu  
 35 40 45

|   |     |
|---|-----|
| ggg aac gtg ctg acc ttg ggc aag agc ccc cac ctg gcg ctg tcc agg | 251 |
| Gly Asn Val Leu Thr Leu Gly Lys Ser Pro His Leu Ala Leu Ser Arg |     |
| 50 55 60  |     |
| ctg agc cag cgt tat ggg gac gtg ctg cag atc cgc atc ggc tcc acc | 299 |
| Leu Ser Gln Arg Tyr Gly Asp Val Leu Gln Ile Arg Ile Gly Ser Thr |     |
| 65 70 75  |     |
| ccc gtg ctg gtg ctc agt ggc ctg gac acc atc cgg cag gcc ctg gtg | 347 |
| Pro Val Leu Val Leu Ser Gly Leu Asp Thr Ile Arg Gln Ala Leu Val |     |
| 80 85 90 95   |     |
| cgc cag ggg gat gat ttc aag ggc cgg ccc gac ctc tac agc ttc tct | 395 |
| Arg Gln Gly Asp Asp Phe Lys Gly Arg Pro Asp Leu Tyr Ser Phe Ser |     |
| 100 105 110   |     |
| ctg gtg acc gac ggc caa agc ctg acc ttc agc cca gac tcc gga cca | 443 |
| Leu Val Thr Asp Gly Gln Ser Leu Thr Phe Ser Pro Asp Ser Gly Pro |     |
| 115 120 125   |     |
| gtg tgg gct gcg cgc agg cgc ctg gct cag aac gcg ctc aac acc ttc | 491 |
| Val Trp Ala Ala Arg Arg Leu Ala Gln Asn Ala Leu Asn Thr Phe     |     |
| 130 135 140   |     |
| tcc att gcc tcc gac ccg gct tcc tcg tgc tct tgc tac ctg gaa gag | 539 |
| Ser Ile Ala Ser Asp Pro Ala Ser Ser Cys Ser Cys Tyr Leu Glu Glu |     |
| 145 150 155   |     |
| cat gtg agc aag gag gcc gag gcc ctt ctc agc agg ctg cag gag cag | 587 |
| His Val Ser Lys Glu Ala Glu Ala Leu Leu Ser Arg Leu Gln Glu Gln |     |
| 160 165 170 175   |     |
| atg gca gag gtt ggg cgc ttt gat ccc tac aac caa gtg ctg atg tca | 635 |
| Met Ala Glu Val Gly Arg Phe Asp Pro Tyr Asn Gln Val Leu Met Ser |     |
| 180 185 190   |     |
| gtg gcc aat gtc att ggt gca atg tgc ttt ggg cac cac ttc tct cag | 683 |
| Val Ala Asn Val Ile Gly Ala Met Cys Phe Gly His His Phe Ser Gln |     |
| 195 200 205   |     |
| aga agt gag gaa atg ctc ccc ctc cta atg agc tcc agt gat ttt gtg | 731 |
| Arg Ser Glu Glu Met Leu Pro Leu Leu Met Ser Ser Asp Phe Val     |     |
| 210 215 220   |     |
| gag acc gtc tcc aac ggg aac ccg gtg gac ttt ttc ccc att ctc caa | 779 |
| Glu Thr Val Ser Asn Gly Asn Pro Val Asp Phe Phe Pro Ile Leu Gln |     |
| 225 230 235   |     |

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|---|-----|-----|-----|-----|------|
| tat atg ccc aac tca gcc ctg cag aga ttc aag aac ttc aac cag acg | 240 | 245 | 250 | 255 | 827  |
| Tyr Met Pro Asn Ser Ala Leu Gln Arg Phe Lys Asn Phe Asn Gln Thr |     |     |     |     |      |
| ttc gtg cag tcc ctg cag aaa att gtc cag gaa cac tat caa gac ttt | 260 | 265 | 270 |     | 875  |
| Phe Val Gln Ser Leu Gln Lys Ile Val Gln Glu His Tyr Gln Asp Phe |     |     |     |     |      |
| gat gag cgc agt gtc cag gac atc aca ggc gcc ctc ttg aag cac aat | 275 | 280 | 285 |     | 923  |
| Asp Glu Arg Ser Val Gln Asp Ile Thr Gly Ala Leu Leu Lys His Asn |     |     |     |     |      |
| gag aag agc tcc agg gct agt gat ggc cac atc ccc caa gag aag att | 290 | 295 | 300 |     | 971  |
| Glu Lys Ser Ser Arg Ala Ser Asp Gly His Ile Pro Gln Glu Lys Ile |     |     |     |     |      |
| gtc aac ctt atc aac gac att ttt ggg gcc gga ttt gac act gtc aca | 305 | 310 | 315 |     | 1019 |
| Val Asn Leu Ile Asn Asp Ile Phe Gly Ala Gly Phe Asp Thr Val Thr |     |     |     |     |      |
| acg gcc att tcc tgg agt ctt atg tac ctt gtg gca aac cct gag ata | 320 | 325 | 330 | 335 | 1067 |
| Thr Ala Ile Ser Trp Ser Leu Met Tyr Leu Val Ala Asn Pro Glu Ile |     |     |     |     |      |
| cag aga aag atc cag aag gag ttg gac acg gtg att ggc agg gca cgg | 340 | 345 | 350 |     | 1115 |
| Gln Arg Lys Ile Gln Lys Glu Leu Asp Thr Val Ile Gly Arg Ala Arg |     |     |     |     |      |
| cag cct cgc ctc tct gac agg ccc cag ctg ccc tta atg gag gcc ttc | 355 | 360 | 365 |     | 1163 |
| Gln Pro Arg Leu Ser Asp Arg Pro Gln Leu Pro Leu Met Glu Ala Phe |     |     |     |     |      |
| atc ctg gag atc ttc cga cac acc tcc ttt gtc ccc ttc acc atc ccc | 370 | 375 | 380 |     | 1211 |
| Ile Leu Glu Ile Phe Arg His Thr Ser Phe Val Pro Phe Thr Ile Pro |     |     |     |     |      |
| cac agc aca aca aag gac aca acc tta aag ggc ttc tac atc ccc aag | 385 | 390 | 395 |     | 1259 |
| His Ser Thr Thr Lys Asp Thr Thr Leu Lys Gly Phe Tyr Ile Pro Lys |     |     |     |     |      |
| gaa tgc tgt gtc ttc ata aac cag tgg cag gtc aat cat gac caa sag | 400 | 405 | 410 | 415 | 1307 |
| Glu Cys Cys Val Phe Ile Asn Gln Trp Gln Val Asn His Asp Gln Xaa |     |     |     |     |      |
| gtg tgg ggg gat cca ttt gca ttc cgg cca gag cga ttc ctc act gca | 420 | 425 | 430 |     | 1355 |
| Val Trp Gly Asp Pro Phe Ala Phe Arg Pro Glu Arg Phe Leu Thr Ala |     |     |     |     |      |

|   |     |      |     |
|---|-----|------|-----|
| gat ggy acc rcc atc aac aag acc ttg agt gag aag gtg atg ctc ttt |     | 1403 |     |
| Asp Xaa Thr Xaa Ile Asn Lys Thr Leu Ser Glu Lys Val Met Leu Phe |     |      |     |
| 435   | 440 | 445  |     |
| ggc atg ggc aag cgc cgg tgc ata gga gag gtc ctg gcc aag tgg gag |     | 1451 |     |
| Gly Met Gly Lys Arg Arg Cys Ile Gly Glu Val Leu Ala Lys Trp Glu |     |      |     |
| 450   | 455 | 460  |     |
| atc ttc ctc ttc cta gcc atc ttg ctg cag cgg ctg gag ttc agc gtg |     | 1499 |     |
| Ile Phe Leu Phe Leu Ala Ile Leu Leu Gln Arg Leu Glu Phe Ser Val |     |      |     |
| 465   | 470 | 475  |     |
| cca gca ggt gtg aaa gta gac cta acc ccc atc tat ggg ctg acc atg |     | 1547 |     |
| Pro Ala Gly Val Lys Val Asp Leu Thr Pro Ile Tyr Gly Leu Thr Met |     |      |     |
| 480   | 485 | 490  | 495 |
| aag cac acc cgc tgt gag cat gtc cag gca cgg cca cgc ttc tcc atc |     | 1595 |     |
| Lys His Thr Arg Cys Glu His Val Gln Ala Arg Pro Arg Phe Ser Ile |     |      |     |
| 500   | 505 | 510  |     |
| aag tga aggcaccagc atgycaaggc agagggagga gaaggat                |     | 1638 |     |
| Lys   |     |      |     |

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 <222> (415).. (415)  
 <223> The 'Xaa' at location 415 stands for Glu or Gln.

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 <222> (433).. (433)  
 <223> The 'Xaa' at location 433 stands for Gly.

<220>  
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 <222> (435).. (435)  
 <223> The 'Xaa' at location 435 stands for Ala or Thr.

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Phe Cys Leu Val Leu Trp Val Val Lys Ala Trp Gln Pro Arg Leu Pro  
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Lys Gly Leu Lys Ser Pro Pro Gly Pro Trp Gly Trp Pro Leu Leu Gly  
35 40 45

Asn Val Leu Thr Leu Gly Lys Ser Pro His Leu Ala Leu Ser Arg Leu  
50 55 60

Ser Gln Arg Tyr Gly Asp Val Leu Gln Ile Arg Ile Gly Ser Thr Pro  
65 70 75 80

Val Leu Val Leu Ser Gly Leu Asp Thr Ile Arg Gln Ala Leu Val Arg  
85 90 95

Gln Gly Asp Asp Phe Lys Gly Arg Pro Asp Leu Tyr Ser Phe Ser Leu  
100 105 110

Val Thr Asp Gly Gln Ser Leu Thr Phe Ser Pro Asp Ser Gly Pro Val  
115 120 125

Trp Ala Ala Arg Arg Arg Leu Ala Gln Asn Ala Leu Asn Thr Phe Ser  
130 135 140

Ile Ala Ser Asp Pro Ala Ser Ser Cys Ser Cys Tyr Leu Glu Glu His  
145 150 155 160

Val Ser Lys Glu Ala Glu Ala Leu Leu Ser Arg Leu Gln Glu Gln Met  
165 170 175

Ala Glu Val Gly Arg Phe Asp Pro Tyr Asn Gln Val Leu Met Ser Val  
180 185 190

Ala Asn Val Ile Gly Ala Met Cys Phe Gly His His Phe Ser Gln Arg  
195 200 205

Ser Glu Glu Met Leu Pro Leu Leu Met Ser Ser Ser Asp Phe Val Glu  
210 215 220

Thr Val Ser Asn Gly Asn Pro Val Asp Phe Phe Pro Ile Leu Gln Tyr  
225 230 235 240

Met Pro Asn Ser Ala Leu Gln Arg Phe Lys Asn Phe Asn Gln Thr Phe  
245 250 255

Val Gln Ser Leu Gln Lys Ile Val Gln Glu His Tyr Gln Asp Phe Asp  
260 265 270

Glu Arg Ser Val Gln Asp Ile Thr Gly Ala Leu Leu Lys His Asn Glu  
275 280 285

Lys Ser Ser Arg Ala Ser Asp Gly His Ile Pro Gln Glu Lys Ile Val  
290 295 300

Asn Leu Ile Asn Asp Ile Phe Gly Ala Gly Phe Asp Thr Val Thr Thr  
305 310 315 320

Ala Ile Ser Trp Ser Leu Met Tyr Leu Val Ala Asn Pro Glu Ile Gln  
325 330 335

Arg Lys Ile Gln Lys Glu Leu Asp Thr Val Ile Gly Arg Ala Arg Gln  
340 345 350

Pro Arg Leu Ser Asp Arg Pro Gln Leu Pro Leu Met Glu Ala Phe Ile  
355 360 365

Leu Glu Ile Phe Arg His Thr Ser Phe Val Pro Phe Thr Ile Pro His  
370 375 380

Ser Thr Thr Lys Asp Thr Thr Leu Lys Gly Phe Tyr Ile Pro Lys Glu  
385 390 395 400

Cys Cys Val Phe Ile Asn Gln Trp Gln Val Asn His Asp Gln Xaa Val  
405 410 415

Trp Gly Asp Pro Phe Ala Phe Arg Pro Glu Arg Phe Leu Thr Ala Asp  
420 425 430

Xaa Thr Xaa Ile Asn Lys Thr Leu Ser Glu Lys Val Met Leu Phe Gly  
435 440 445

Met Gly Lys Arg Arg Cys Ile Gly Glu Val Leu Ala Lys Trp Glu Ile  
450 455 460

Phe Leu Phe Leu Ala Ile Leu Leu Gln Arg Leu Glu Phe Ser Val Pro  
465 470 475 480

Ala Gly Val Lys Val Asp Leu Thr Pro Ile Tyr Gly Leu Thr Met Lys  
485 490 495

His Thr Arg Cys Glu His Val Gln Ala Arg Pro Arg Phe Ser Ile Lys  
500 505 510